

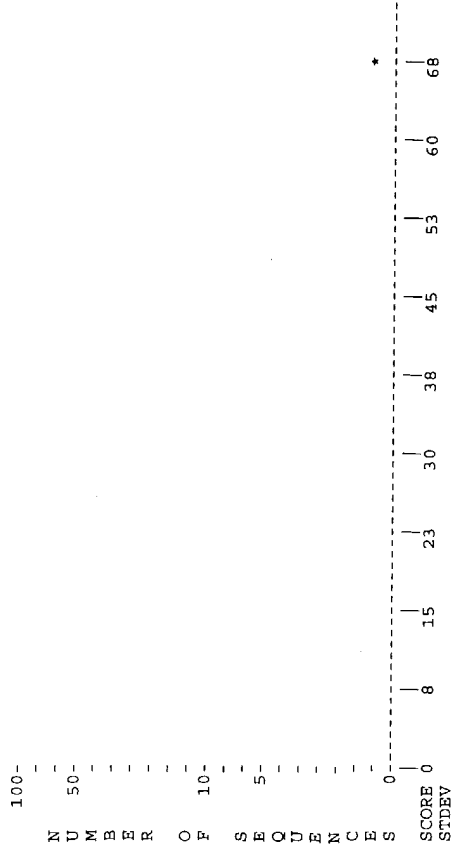
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IntelliGenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 069434_4_x_m33987_inv.res made by spaula on Wed 22 Sep 104 12:49:06-PST.

Query sequence being compared: US-10-069-434-4' (1-911)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-10-069-434-4' (1-911) with:
File : m33987.seq



PARAMETERS

Similarity matrix Unitary K-tuple 4
Mismatch penalty 1 Joining penalty 30
Gap penalty 1.00 Window size 500
Gap size penalty 0.33
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
68 0 0.00
Times: CPU 00:00:00.00 Total Elapsed
00:00:00.00

Number of residues: 2785
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name Description Length Score Score Init. Opt.
1. m33987 TOIG of: m33987 check: 7224 from: 1 to: 2785 68 410 0.00 0

US-10-069-434-4' (1-911)
TOIG of: m33987 check: 7224 from: 1 to: 2785

TOIG of: m33987 check: 7224 from: 1 to: 2785

LOCUS HUMCAIX
DEFINITION Human carbonic anhydrase I (CAI) mRNA, complete cds.
ACCESSION M33987
VERSION M33987.1 GI:179792
KEYWORDS carbonic anhydrase I.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2785)
AUTHORS Lowe,N., Brady,H.J., Barlow,J.H., Sowden,J.C., Edwards,M. and Butterworth,P.H.
TITLE Structure and methylation patterns of the gene encoding human carbonic anhydrase I
JOURNAL Gene 93 (2), 277-283 (1990)
MEDLINE 91033039
PubMed 2121614

COMMENT
Original source text: Human EBV transformed SH B cell line DNA, and cDNA to mRNA.
Since no intron sequences were provided this entry is treated as if originating from an mRNA.
Draft entry and computer-readable sequence for [Unpublished (1990)] kindly submitted
by N.Lowe, 09-MAY-1990.
Author address: N.Lowe
Department of Biochemistry
University College London
Gower Street, London
WC1E 6BT, U.K.
E-mail: UCBMWAR@UCLID.UCL.AC.UK@CUNYVM.CUNY.EDU.

FEATURES

Source
1..2785
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/map="8q13-q22"
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874..879
/gene="CA1"
902..2165
/gene="CA1"
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902..1939
/gene="CA1"
/note="carbonic anhydrase I mRNA (alt.)"
1048..1833
/gene="CA1"
/note="carbonic anhydrase I (EC 4.2.1.1)"
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/protein_id="AA51910.1"
/db_xref="GI:179793"
/db_xref="GDB:G00-119-047"
/translation="MASPDWGYDDKNGPEQWSKLYPIANGNNQSPVDIKTSEKHDTS
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VLDALQAIKTKGRAPETNPDPSTLLPSSLDFTWYPSGLTHPPPLVESVTWICKRESIS
VSSQOLAQFRSLLSNVEGDNAVPMQHNNRPTQPLKGRTRASF"

ORIGIN

M33987 Length: 2785 September 22, 2004 12:44 Type: N Check: 7224

Initial Score = 68 Optimized Score = 410 Significance = 0.00
 Residue Identity = 50% Matches = 535 Mismatches = 329
 Gaps = 201 Conservative Substitutions = 0

670 680 690 700 710 720 730
 CAGTTTCCTCTCTTGAGCAGCTGATTAAATCCACACCCCAACCACTTCCCTTATCAGGTTCTCACACTCTGG
 X
 TTTTTC--CCCTTGGCAATT-TGG
 20 30 40 50 60 70 80
 GAAAAAGTCAATG---CCAGTGGTTCAGAGCTCTGAGGCTGAGGTGGGAGGATCA---CTTGAGTCCAGGAGTT
 GGCRACT-ATGTACCACACT-CTAATCCACACAGGCGCCAGACATCAGACAAATTAAAGACAGCGCCCATGCCCC
 740 750 760 770 780 790 800
 90 100 110 120 130 140 150
 GGAGGCTGC---AAATTAGCCAAAGATTGTACCACTGCCCTCCAGCCTGGGTGACAGAGTGAGACTCTAT--CA
 AAAGCCCGCAAAATATGCAA-ATTAT--TCAAATATTCAACCTAGCTAAC---CCCAACCTTTTTCGTG
 810 820 830 840 850 860 870
 160 170 180 190
 CAGAAAAGCTGTGCTTCAACCTCC--GC-TGTG-----CA-----CAGGAG--AC-----TGC---GAAATTT
 TACATAAGCTGCCCATTCCTCCCTCCAGCCTGTGGTACCCAGTCTCAGGTGCAACCCCTCGGTGGTCTCT
 880 890 900 910 920 930 940
 210 220 230 240 250
 G-GCCAGC-----TGTGAGAGCTGATGT--TTATAGTGTGCTTTAAACAA-----TCCATGTGACA
 GTGGCAGCCTTCTCTCATTTCAGAGCTGTTTTCACAGAGGTAG--TGAAGAAGAACTGGATTTTCAAGT--TCA
 260 270 280 290 300 310 320
 CTCT--CAAGAAGAGTGGAACTGTAAAG-AGAACCAGGAT-ATGTCCAGTAGTCCCGAGGATGGTG-GAAGCAG
 CTTTGAAG-AGAAAAGAAACTCAGTAGAA---GATAATGGCAAGT---CCAGACTGGGATATGATG
 1020 1030 1040 1050 1060 1070
 330 340 350 360 370 380 390
 AGACAAATAGTCAAAATTTGTGAATCGAGTTCTTTACCTTTCTTTAATGAA--TCCAAAGTGTGAG-T
 ACAAAAATGGTCTGTAACATGAGCAAG-CTGTAT--CCCATGTC--CAATGGAATAACCAATCCCTGTT
 1080 1090 1100 1110 1120 1130 1140
 400 410 420 430 440 450
 AATCTT--TTGCAAT--TGGGAATTAGGTTCAACCAATCTGTAA--AAACA-----CTCC--CAAGACAGC--C
 GATATTAACCAACAGTGAACCAACATG-ACACTCTCTGAAACCTATTAGTGTCTCTCAACACCAACCGAT--CAGTG
 1150 1160 1170 1180 1190 1200 1210
 460 470 480 490 500 510
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 1220 1230 1240 1250 1260 1270 1280
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 CTGAAAGGTGGTCTCTCTGACAGCTACAGGCTCTTTCAGTTTCAATTTTCACT--GGGCGAGTACAAATGA
 1290 1300 1310 1320 1330 1340 1350
 520 530 540 550 560 570
 GC--GG-----ACCCCGAGT-GAAGTGT--AA-----CTTCCGCTAACCT---GTAGCTCCAGTGAGAGGA
 GCATGGTTCAGAACATACAGTGGATGAGTCAATATTCTGGCG-AGCTTCAGGTAGCT--CACTG-GAAT
 1360 1370 1380 1390 1400 1410 1420
 580 590 600 610 620 630
 CCACCCAGCAACTGATTTGTCTCTGTGTATCAAG--TCACATT--GAAGGAATGCCGCTGTGCT
 640 650 660 670 680 690
 1020 1030 1040 1050 1060 1070
 330 340 350 360 370 380 390
 AGACAAATAGTCAAAATTTGTGAATCGAGTTCTTTACCTTTCTTTAATGAA--TCCAAAGTGTGAG-T
 ACAAAAATGGTCTGTAACATGAGCAAG-CTGTAT--CCCATGTC--CAATGGAATAACCAATCCCTGTT
 1080 1090 1100 1110 1120 1130 1140
 400 410 420 430 440 450
 AATCTT--TTGCAAT--TGGGAATTAGGTTCAACCAATCTGTAA--AAACA-----CTCC--CAAGACAGC--C
 GATATTAACCAACAGTGAACCAACATG-ACACTCTCTGAAACCTATTAGTGTCTCTCAACACCAACCGAT--CAGTG
 1150 1160 1170 1180 1190 1200 1210
 460 470 480 490 500 510
 AGTCCATCTGGT--TCA-TGAGTGTGCT-----CA-ACAAAGCTGGGATTTGTCTGA---ATTCCAGTG
 AGCAAAGAAATATCAATGTGGGGATTTCTTCCATGTAAATTTTGGAGACCAACGATACCGAT--CAGTG
 1220 1230 1240 1250 1260 1270 1280
 -AACACATGG-----AGCTCTG-CAGC-ATA-GCTCACTCCATCTACTATGTGCTCGGAGCCGTGGTCATCA
 CTGAAAGGTGGTCTCTCTGACAGCTACAGGCTCTTTCAGTTTCAATTTTCACT--GGGCGAGTACAAATGA
 1290 1300 1310 1320 1330 1340 1350
 520 530 540 550 560 570
 GC--GG-----ACCCCGAGT-GAAGTGT--AA-----CTTCCGCTAACCT---GTAGCTCCAGTGAGAGGA
 GCATGGTTCAGAACATACAGTGGATGAGTCAATATTCTGGCG-AGCTTCAGGTAGCT--CACTG-GAAT
 1360 1370 1380 1390 1400 1410 1420
 580 590 600 610 620 630
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 640 650 660 670 680 690

CTGCAAAAGTACTCCAGCCTTGCTGAAGCTG-CCTCAAAAGGCTGATGGTTTGGCACTTATTGGTG-TTTTGAT
 1430 1440 1450 1460 1470 1480 1490
 700 710 720 730 740
 GATGATT--TTAG-----CTGAGCTTGGGTCA-TACTTGAT-----ACTAAGTGGT-----CGGAGGG---
 GAAAGTTGGTGAAGGCCAACCCCAAGCTGCAGAAAGTACTTGAATGCCCTCCCAAGCAATTAACCAAGGCGCAA
 1500 1510 1520 1530 1540 1550 1560
 750 760 770 780 790 800
 AAGAGTCATATTCTCTTCTTTGG-----TTTTAATCTCAAT--TGA-----GATTGCTGATC--ACCATC
 ACGAGCCCCA-TTCACAAATTTTGACCCCTCTACTCTCTCTTCTCATCCCTGGATTTCTGGACCTACCT-
 1570 1580 1590 1600 1610 1620 1630
 810 820 830 840 850 860 870
 AGCAATAGGGAATAATTCCTTCAGTGAATAGACCGTGTGTCTCGCGTATC-CCCAGCTGAGCCTCGACA
 GGCTCT-CTGACTCAT-CCT-CCTCT--TTATGAGAGTGAACCTTGGATCATCTGTGAAGGAGAGCAT----CA
 1640 1650 1660 1670 1680 1690
 880 890 900 X
 TGGTC-CCTCGGGTGGAACTCGAGCCGAAATTCGG
 GTGTGAGTCTC--AGAGCAGCT--GGCAAAATTCGAGCCTTCTATCAAAATGTTGAAGGTGATAACGCTGTC
 1700 1710 1720 1730 1740 1750 1760
 CCCATGCGACACA
 1770 1780